



SEQUENCE LISTING

<110> Sukhapiinda, Kitisri
Hasler, James M
Petell, James K
Strickland, James A
Folkerts, Otto

<120> ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS

<130> 50447

<140> US 09/358,321

<141> 1999-07-21

<150> US 60/093,587

<151> 1998-07-21

<160> 56

<170> PatentIn Ver. 2.0

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5' primer

<220>

<221> unsure

<222> (12)

<223> n can be a,t,g, or c in this degenerate primer

<400> 1

gargaraaym gncaygg

17

<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' primer

<220>

<221> unsure

<222> (7)

<223> n can be a,t,g, or c in this degenerate primer

<400> 2

ytcrtgncy ttytcrtc

18

<210> 3

<211> 276

<212> DNA

<213> Zea mays

<220>
 <221> CDS
 <222> (1)..(276)

<400> 3

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| gag gag aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act | 48 |
| Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr | |
| 1 5 10 15 | |
| ggg agg gtg gat atg agg cag att gag aag aca att cag tat ctt att | 96 |
| Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile | |
| 20 25 30 | |
| ggc tct gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc | 144 |
| Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe | |
| 35 40 45 | |
| atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac ggg aac | 192 |
| Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn | |
| 50 55 60 | |
| act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca caa atc | 240 |
| Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile | |
| 65 70 75 80 | |
| tgc ggc atc atc gcc tca gat gag aag cga cat gaa | 276 |
| Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu | |
| 85 90 | |

<210> 4
 <211> 92
 <212> PRT
 <213> Zea mays

<400> 4

| | |
|---|--|
| Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr | |
| 1 5 10 15 | |
| Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile | |
| 20 25 30 | |
| Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe | |
| 35 40 45 | |
| Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn | |
| 50 55 60 | |
| Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile | |
| 65 70 75 80 | |
| Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu | |
| 85 90 | |

<210> 5
 <211> 1621
 <212> DNA
 <213> Zea mays

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<220>
<221> mat_peptide
<222> (239)..(1324)
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3

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| ctc act ggg agg gtg gat atg agg cag att gag aag aca att cag tat | 748 |
| Leu Thr Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr | |
| 155 160 165 170 | |
| ctt att ggc tct gga atg gat cct agg act gag aat aat cct tat ctt | 796 |
| Leu Ile Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu | |
| 175 180 185 | |
| ggt ttc atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac | 844 |
| Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His | |
| 190 195 200 | |
| ggg aac act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca | 892 |
| Gly Asn Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala | |
| 205 210 215 | |
| caa atc tgc ggc atc atc gcc tca gat gag aag cga cat gaa act gcg | 940 |
| Gln Ile Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala | |
| 220 225 230 | |
| tac acc aag atc gtg gag aag ctg ttt gag atc gac cct gat ggt acc | 988 |
| Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr | |
| 235 240 245 250 | |
| gtg gtc gct ctg gct gac atg atg agg aag aag atc tca atg cct gcc | 1036 |
| Val Val Ala Leu Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala | |
| 255 260 265 | |
| cac ctg atg ttt gac ggg cag gac gac aag ctg ttc gag cac ttc tcc | 1084 |
| His Leu Met Phe Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser | |
| 270 275 280 | |
| atg gtc gcg cag agg ctt ggc gtt tac acc gcc agg gac tac gcc gac | 1132 |
| Met Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp | |
| 285 290 295 | |
| atc ctc gag ttc ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt | 1180 |
| Ile Leu Glu Phe Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly | |
| 300 305 310 | |
| ctg tcg ggt gaa ggg aac aag gcg cag gac tac ctt tgc acc ctt gct | 1228 |
| Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala | |
| 315 320 325 330 | |
| tca aga atc agg agg ctg gag gag agg gcc cag agc aga gcc aag aaa | 1276 |
| Ser Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys | |
| 335 340 345 | |
| gcc ggc acg ctg cct ttc agc tgg gta tac ggt agg gac gtc caa ctg | 1324 |
| Ala Gly Thr Leu Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu | |
| 350 355 360 | |
| tgagatcgga aacctgctgc ggactgctta gacaagacct gctgtgtctg cgttacatag | 1384 |
| gtctccaggt tttgatcaaa tgggtcccggtg tcgtcttata gagcgatagg agaacgtgtt | 1444 |
| ggctctgtggt gtagctttgt ttttatttttg tattttttctg ctttggatgta caacctgtgg | 1504 |
| ccgcatgaac tggggcggtgg agatgggagc gaccatgccg tactttgtct gtcgctggcg | 1564 |
| gtgtgttttcg gtatgttatt tgagttgctc agatctgtta aaaaaaaaaa aaaaaaa | 1621 |

<210> 6
 <211> 393
 <212> PRT
 <213> Zea mays

<400> 6

| | | | | | | | | | | | | | | | | | | |
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| Met | Ala | Leu | Arg | Leu | Asn | Asp | Val | Ala | Leu | Cys | Leu | Ser | Pro | Pro | Leu | -30 | -25 | -20 |
| Ala | Ala | Arg | Arg | Arg | Arg | Arg | Ser | Ser | Gly | Arg | Phe | Val | Ala | Val | Ala | -15 | -10 | -5 |
| Ser | Met | Thr | Ser | Ala | Val | Ser | Thr | Lys | Val | Glu | Asn | Lys | Lys | Pro | Phe | 5 | 10 | 15 |
| Ala | Pro | Pro | Arg | Glu | Val | His | Val | Gln | Val | Thr | His | Ser | Met | Pro | Pro | 20 | 25 | 30 |
| His | Lys | Ile | Glu | Ile | Phe | Lys | Ser | Leu | Asp | Asp | Trp | Ala | Arg | Asp | Asn | 35 | 40 | 45 |
| Ile | Leu | Thr | His | Leu | Lys | Pro | Val | Glu | Lys | Cys | Trp | Gln | Pro | Gln | Asp | 50 | 55 | 60 |
| Phe | Leu | Pro | Asp | Pro | Ala | Ser | Glu | Gly | Phe | His | Asp | Glu | Val | Lys | Glu | 70 | 75 | 80 |
| Leu | Arg | Glu | Arg | Ala | Lys | Glu | Ile | Pro | Asp | Asp | Tyr | Phe | Val | Cys | Leu | 85 | 90 | 95 |
| Val | Gly | Asp | Met | Ile | Thr | Glu | Glu | Ala | Leu | Pro | Thr | Tyr | Gln | Thr | Met | 100 | 105 | 110 |
| Leu | Asn | Thr | Leu | Asp | Gly | Val | Arg | Asp | Glu | Thr | Gly | Ala | Ser | Pro | Thr | 115 | 120 | 125 |
| Ala | Trp | Ala | Val | Trp | Thr | Arg | Ala | Trp | Thr | Ala | Glu | Glu | Asn | Arg | His | 130 | 135 | 140 |
| Gly | Asp | Leu | Leu | Asn | Lys | Tyr | Met | Tyr | Leu | Thr | Gly | Arg | Val | Asp | Met | 150 | 155 | 160 |
| Arg | Gln | Ile | Glu | Lys | Thr | Ile | Gln | Tyr | Leu | Ile | Gly | Ser | Gly | Met | Asp | 165 | 170 | 175 |
| Pro | Arg | Thr | Glu | Asn | Asn | Pro | Tyr | Leu | Gly | Phe | Ile | Tyr | Thr | Ser | Phe | 180 | 185 | 190 |
| Gln | Glu | Arg | Ala | Thr | Phe | Ile | Ser | His | Gly | Asn | Thr | Ala | Arg | His | Ala | 195 | 200 | 205 |
| Lys | Asp | Phe | Gly | Asp | Leu | Lys | Leu | Ala | Gln | Ile | Cys | Gly | Ile | Ile | Ala | 210 | 215 | 220 |
| Ser | Asp | Glu | Lys | Arg | His | Glu | Thr | Ala | Tyr | Thr | Lys | Ile | Val | Glu | Lys | 230 | 235 | 240 |
| Leu | Phe | Glu | Ile | Asp | Pro | Asp | Gly | Thr | Val | Val | Ala | Leu | Ala | Asp | Met | 245 | 250 | 255 |

Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln
260 265 270

Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly
275 280 285

Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp
290 295 300 305

Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys
310 315 320

Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Glu
325 330 335

Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser
340 345 350

Trp Val Tyr Gly Arg Asp Val Gln Leu
355 360

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
atggctagcc tccgcctcaa cgacgtcgcg 30

<210> 8
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8
aaagctagct catcacagtt ggacgtccct accgta 36

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
accatggcta gcatgacgtc cgccgtctcc 30

<210> 10
<211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 10
 gatgatgcta gctcacagtt ggacgtccct 30

<210> 11
 <211> 1107
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (4)..(1092)

<400> 11
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 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys
 1 5 10 15

aag cca ttt gct cct cca agg gag gta cat gtc cag gtt aca cat tca 96
 Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser
 20 25 30

atg cca cct cac aag att gaa att ttc aag tcg ctt gat gat tgg gct 144
 Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala
 35 40 45

aga gat aat atc ttg acg cat ctc aag cca gtc gag aag tgt tgg cag 192
 Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln
 50 55 60

cca cag gat ttc ctc ccg gac cca gca tct gaa gga ttt cat gat gaa 240
 Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu
 65 70 75

gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct gat gat tat ttt 288
 Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe
 80 85 90 95

gtt tgt ttg gtg gga gac atg att acc gag gaa gct cta cca aca tac 336
 Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
 100 105 110

cag act atg ctt aac acc ctc gac ggt gtc aga gat gag aca ggt gca 384
 Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
 115 120 125

agc ccc act gcc tgg gct gtt tgg acg agg gca tgg act gct gag gag 432
 Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu
 130 135 140

aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act ggg agg 480
 Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg
 145 150 155

gtg gat atg agg cag att gag aag aca att cag tat ctt att ggc tct 528

| | | | | | | | | | | | | | | | | |
|------------|-----|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| Val 160 | Asp | Met | Arg | Gln | Ile 165 | Glu | Lys | Thr | Ile | Gln 170 | Tyr | Leu | Ile | Gly | Ser 175 | |
| gga | atg | gat | cct | agg | act | gag | aat | aat | cct | tat | ctt | ggt | ttc | atc | tac | 576 |
| Gly | Met | Asp | Pro | Arg 180 | Thr | Glu | Asn | Asn | Pro 185 | Tyr | Leu | Gly | Phe | Ile 190 | Tyr | |
| acc | tcc | ttc | caa | gag | cgg | gcg | acc | ttc | atc | tca | cac | ggg | aac | act | gct | 624 |
| Thr | Ser | Phe | Gln 195 | Glu | Arg | Ala | Thr | Phe | Ile 200 | Ser | His | Gly | Asn 205 | Thr | Ala | |
| cgt | cac | gcc | aag | gac | ttt | ggc | gac | tta | aag | ctt | gca | caa | atc | tgc | ggc | 672 |
| Arg | His | Ala 210 | Lys | Asp | Phe | Gly | Asp 215 | Leu | Lys | Leu | Ala | Gln 220 | Ile | Cys | Gly | |
| atc | atc | gcc | tca | gat | gag | aag | cga | cat | gaa | act | gcg | tac | acc | aag | atc | 720 |
| Ile | Ile | Ala 225 | Ser | Asp | Glu | Lys | Arg 230 | His | Glu | Thr | Ala 235 | Tyr | Thr | Lys | Ile | |
| gtg | gag | aag | ctg | ttt | gag | atc | gac | cct | gat | ggt | acc | gtg | gtc | gct | ctg | 768 |
| Val | Glu | Lys | Leu | Phe | Glu 245 | Ile | Asp | Pro | Asp | Gly 250 | Thr | Val | Val | Ala | Leu 255 | |
| gct | gac | atg | atg | agg | aag | aag | atc | tca | atg | cct | gcc | cac | ctg | atg | ttt | 816 |
| Ala | Asp | Met | Met | Arg 260 | Lys | Lys | Ile | Ser | Met 265 | Pro | Ala | His | Leu | Met 270 | Phe | |
| gac | ggg | cag | gac | gac | aag | ctg | ttc | gag | cac | ttc | tcc | atg | gtc | gcg | cag | 864 |
| Asp | Gly | Gln | Asp 275 | Asp | Lys | Leu | Phe | Glu | His 280 | Phe | Ser | Met | Val 285 | Ala | Gln | |
| agg | ctt | ggc | gtt | tac | acc | gcc | agg | gac | tac | gcc | gac | atc | ctc | gag | ttc | 912 |
| Arg | Leu | Gly 290 | Val | Tyr | Thr | Ala | Arg 295 | Asp | Tyr | Ala | Asp | Ile 300 | Leu | Glu | Phe | |
| ctc | gtc | gac | agg | tgg | aag | gtg | gcg | agc | ctg | act | ggt | ctg | tcg | ggt | gaa | 960 |
| Leu | Val | Asp | Arg | Trp | Lys 305 | Val | Ala 310 | Ser | Leu | Thr | Gly 315 | Leu | Ser | Gly | Glu | |
| ggg | aac | aag | gcg | cag | gac | tac | ctt | tgc | acc | ctt | gct | tca | aga | atc | agg | 1008 |
| Gly | Asn | Lys | Ala | Gln | Asp 325 | Tyr | Leu | Cys | Thr | Leu 330 | Ala | Ser | Arg | Ile 335 | Arg | |
| agg | ctg | gag | gag | agg | gcc | cag | agc | aga | gcc | aag | aaa | gcc | ggc | acg | ctg | 1056 |
| Arg | Leu | Glu | Glu | Arg 340 | Ala | Gln | Ser | Arg | Ala 345 | Lys | Lys | Ala | Gly | Thr 350 | Leu | |
| cct | ttc | agc | tgg | gta | tac | ggt | agg | gac | gtc | caa | ctg | tgagctagca | tcac | | | 1107 |
| Pro | Phe | Ser | Trp 355 | Val | Tyr | Gly | Arg | Asp 360 | Val | Gln | Leu | | | | | |

<210> 12
 <211> 363
 <212> PRT
 <213> Zea mays

<400> 12
 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys
 1 5 10 15

Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met
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 Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg
 35 40 45
 Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro
 50 55 60
 Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val
 65 70 75 80
 Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val
 85 90 95
 Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln
 100 105 110
 Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser
 115 120 125
 Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn
 130 135 140
 Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val
 145 150 155 160
 Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly
 165 170 175
 Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr
 180 185 190
 Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg
 195 200 205
 His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile
 210 215 220
 Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val
 225 230 235 240
 Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala
 245 250 255
 Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp
 260 265 270
 Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg
 275 280 285
 Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu
 290 295 300
 Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly
 305 310 315 320
 Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg
 325 330 335
 Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro

<220>
 <223> Description of Artificial Sequence:primer

 <400> 17
 aaagctagcc tsctgcygyt ctkkttwycw ggtryc 36

 <210> 18
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 18
 tacgttacct gagcgggccgc gctgggctca agttttttgt ccaccg 46

 <210> 19
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 19
 ttgctagct tactaacact cattcctgtt gaagctct 38

 <210> 20
 <211> 102
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 20
 gcactaggtc aatctagaat ggtaagcgt attgttttat atgtgctttt ggcggcggcg 60
 cattctgcct ttgcggcgggt tgtgatgacc ccaaaccac tc 102

 <210> 21
 <211> 738
 <212> DNA
 <213> mouse

 <220>
 <221> unsure
 <222> (16)..(21)
 <223> not known

 <220>
 <221> unsure
 <222> (26)
 <223> not known

 <220>

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<220>
<221> CDS
<222> (37) .. (693)
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| accctcctcc | tggttcnnnnn | ntcagntgtc | ancagtt | gat | ggt | gtg | atg | acc | cca | 54 | | | | | | |
| | | | | Asp | Val | Val | Met | Thr | Pro | | | | | | | |
| | | | | 1 | | | | 5 | | | | | | | | |
| aac | cca | ctc | tcc | ctg | cct | gtc | agt | ctt | gga | gat | caa | gcc | tcc | atc | tct | 102 |
| Asn | Pro | Leu | Ser | Leu | Pro | Val | Ser | Leu | Gly | Asp | Gln | Ala | Ser | Ile | Ser | |
| | | 10 | | | | | | 15 | | | | | 20 | | | |
| tgc | aga | tct | agt | cag | agc | ctt | tta | cac | agt | aat | gga | atc | acc | tat | tta | 150 |
| Cys | Arg | Ser | Ser | Gln | Ser | Leu | Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | |
| | | 25 | | | | | 30 | | | | | 35 | | | | |
| cat | tgg | tac | ctg | cag | aag | cca | ggc | cag | tct | cca | aag | ctc | ctg | atc | tac | 198 |
| His | Trp | Tyr | Leu | Gln | Lys | Pro | Gly | Gln | Ser | Pro | Lys | Leu | Leu | Ile | Tyr | |
| | 40 | | | | | 45 | | | | | 50 | | | | | |
| aaa | ggt | tcc | aac | cga | ttt | tct | ggg | gtc | cca | gac | agg | ttc | agt | ggc | agt | 246 |
| Lys | Val | Ser | Asn | Arg | Phe | Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Gly | Ser | |
| | 55 | | | | 60 | | | | | 65 | | | | | 70 | |
| gga | tca | ggg | aca | gat | ttc | aca | ctc | aag | atc | aac | aga | gtg | gag | gct | gag | 294 |
| Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Lys | Ile | Asn | Arg | Val | Glu | Ala | Glu | |
| | | | | 75 | | | | | 80 | | | | | 85 | | |
| gat | ctg | gga | ggt | tat | ttc | tgc | tct | caa | agt | aca | cat | ggt | ccg | tac | acg | 342 |
| Asp | Leu | Gly | Val | Tyr | Phe | Cys | Ser | Gln | Ser | Thr | His | Val | Pro | Tyr | Thr | |
| | | | 90 | | | | | 95 | | | | | 100 | | | |
| ttc | gga | ggg | ggg | acc | aag | ctg | gaa | ata | aaa | cgg | gct | gat | gct | gca | cca | 390 |
| Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Asp | Ala | Ala | Pro | |
| | | 105 | | | | | 110 | | | | | 115 | | | | |
| act | gta | tcc | atc | ttc | cca | cca | tcc | agt | gag | cag | tta | aca | tct | gga | ggt | 438 |
| Thr | Val | Ser | Ile | Phe | Pro | Pro | Ser | Ser | Glu | Gln | Leu | Thr | Ser | Gly | Gly | |
| | 120 | | | | | 125 | | | | | 130 | | | | | |
| gcc | tca | gtc | gtg | tgc | ttc | ttg | aac | aac | ttc | tac | ccc | aaa | gac | atc | aat | 486 |
| Ala | Ser | Val | Val | Cys | Phe | Leu | Asn | Asn | Phe | Tyr | Pro | Lys | Asp | Ile | Asn | |
| | 135 | | | | 140 | | | | | 145 | | | | | 150 | |
| gtc | aag | tgg | aag | att | gat | ggc | agt | gaa | cga | caa | aat | ggc | gtc | ctg | aac | 534 |
| Val | Lys | Trp | Lys | Ile | Asp | Gly | Ser | Glu | Arg | Gln | Asn | Gly | Val | Leu | Asn | |
| | | | | 155 | | | | | 160 | | | | | 165 | | |
| agt | tgg | act | gat | cag | gac | acc | aaa | gac | agc | acc | tac | agc | atg | agc | agc | 582 |
| Ser | Trp | Thr | Asp | Gln | Asp | Thr | Lys | Asp | Ser | Thr | Tyr | Ser | Met | Ser | Ser | |
| | | | 170 | | | | | 175 | | | | | 180 | | | |
| acc | ctc | acg | ttg | acc | aag | gac | gag | tat | gaa | cga | cat | aac | agc | tat | acc | 630 |
| Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu | Arg | His | Asn | Ser | Tyr | Thr | |
| | | 185 | | | | | 190 | | | | | 195 | | | | |

| | |
|---|-----|
| tgt gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc | 678 |
| Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe | |
| 200 205 210 | |

| | |
|--|-----|
| aac agg aat gag tgt tagtaagcta gcacgcccga tgggtgggacg gtatgaataa | 733 |
| Asn Arg Asn Glu Cys | |
| 215 | |

| | |
|-------|-----|
| tccgg | 738 |
|-------|-----|

<210> 22
 <211> 336
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(336)

| | |
|---|----|
| <400> 22 | |
| gat gtt gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga | 48 |
| Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly | |
| 1 5 10 15 | |

| | |
|---|----|
| gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt | 96 |
| Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser | |
| 20 25 30 | |

| | |
|---|-----|
| aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct | 144 |
| Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser | |
| 35 40 45 | |

| | |
|---|-----|
| cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca | 192 |
| Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro | |
| 50 55 60 | |

| | |
|---|-----|
| gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc | 240 |
| Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile | |
| 65 70 75 80 | |

| | |
|---|-----|
| aac aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt | 288 |
| Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser | |
| 85 90 95 | |

| | |
|---|-----|
| aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa | 336 |
| Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys | |
| 100 105 110 | |

<210> 23
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

| | |
|---|----|
| <400> 23 | |
| gcactaggtc aatctagaat ggtaagcgct attgttttat atgtgctttt ggcggcggcg | 60 |

gcgcattctg cctttgcggc ggttcaactg cagcagctctg gggctgag

108

<210> 24
<211> 882
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (25)..(837)

<220>
<221> mat_peptide
<222> (79)..(837)

<400> 24
ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt 51
Met Thr Ile Leu Cys Trp Leu Ala Leu
-15 -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
-5 -1 1 5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
10 15 20

aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat 195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His
25 30 35

tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa 243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
40 45 50 55

gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
60 65 70

tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat 339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
75 80 85

ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc 387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
90 95 100

gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc 435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly
105 110 115

aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag 483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln
120 125 130 135

cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc 531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser
140 145 150

| | |
|---|-----|
| tgc aag gct tgc ggc tac aca ttt act gac tat gaa ata cac tgg gtg | 579 |
| Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val | |
| 155 160 165 | |
| agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct | 627 |
| Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro | |
| 170 175 180 | |
| gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata | 675 |
| Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile | |
| 185 190 195 | |
| gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc | 723 |
| Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser | |
| 200 205 210 215 | |
| ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag | 771 |
| Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Thr Thr Arg Trp Phe Glu | |
| 220 225 230 | |
| gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct | 819 |
| Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser | |
| 235 240 245 | |
| cat cat cat cat cat cat tagggcctct ctggccgac ccccgattt | 867 |
| His His His His His His | |
| 250 | |
| ccccgatcgt tcaaa | 882 |
| <210> 25 | |
| <211> 339 | |
| <212> DNA | |
| <213> mouse | |
| <220> | |
| <221> CDS | |
| <222> (1)..(339) | |
| <400> 25 | |
| cag gtt gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga | 48 |
| Gln Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly | |
| 1 5 10 15 | |
| gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt | 96 |
| Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser | |
| 20 25 30 | |
| aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct | 144 |
| Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser | |
| 35 40 45 | |
| cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca | 192 |
| Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro | |
| 50 55 60 | |
| gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc | 240 |
| Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile | |
| 65 70 75 80 | |

agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95

aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336
 Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

ggc 339
 Gly

<210> 26
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 26
 cccggggtttg gattcggagc cagatcctga ggatttaccc tctgcagaga cagtgaccag 60
 agtc 64

<210> 27
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 27
 gagggtaaat cctcaggatc tggctccgaa tccaaaccgc gggatgttgt gatgacccca 60
 aac 63

<210> 28
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 28
 gcactaggtc aagcggccgc ttactaatc agatcctctt ctgagatgag tttttcttct 60
 tttatttcca gcttggtc 78

<210> 29
 <211> 459
 <212> DNA
 <213> mouse

<220>

<221> CDS

<222> (19)..(459)

<220>

<221> mat_peptide

<222> (79)..(459)

<400> 29

```
gcactagggtc aatctaga atg gta agc gct att gtt tta tat gtg ctt ttg      51
                      Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu
                      -20                      -15                      -10

gcg gcg gcg gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct      99
Ala Ala Ala Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser
                      -5                      -1      1                      5

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag      147
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys
                      10                      15                      20

gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg cag      195
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln
                      25                      30                      35

aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act      243
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr
                      40                      45                      50                      55

ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act      291
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr
                      60                      65                      70

gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca      339
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr
                      75                      80                      85

tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg      387
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp
                      90                      95                      100

ggc caa ggg act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga      435
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly
                      105                      110                      115

tct ggc tcc gaa tcc aaa ccc ggg
Ser Gly Ser Glu Ser Lys Pro Gly
120                      125
```

<210> 30

<211> 438

<212> DNA

<213> mouse

<220>

<221> CDS

<222> (1)..(408)

<400> 30

```
gag ggt aaa tcc tca gga tct ggc tcc gaa tcc aaa ccc ggg gat gtt      48
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Pro Gly Asp Val
```

| 1 | 5 | 10 | 15 | |
|--|-----|-----|-----|-----|
| gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga gat caa | | | | 96 |
| Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln | | | | |
| | 20 | 25 | 30 | |
| gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt aat gga | | | | 144 |
| Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly | | | | |
| | 35 | 40 | 45 | |
| atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aag | | | | 192 |
| Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys | | | | |
| | 50 | 55 | 60 | |
| ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg | | | | 240 |
| Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg | | | | |
| | 65 | 70 | 75 | 80 |
| ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga | | | | 288 |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg | | | | |
| | 85 | 90 | 95 | |
| gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat | | | | 336 |
| Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His | | | | |
| | 100 | 105 | 110 | |
| gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gaa gaa | | | | 384 |
| Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu Glu | | | | |
| | 115 | 120 | 125 | |
| aaa ctc atc tca gaa gag gat ctg aattagtaag gggccgcctt gacctagtgc | | | | 438 |
| Lys Leu Ile Ser Glu Glu Asp Leu | | | | |
| | 130 | 135 | | |
| <210> 31 | | | | |
| <211> 830 | | | | |
| <212> DNA | | | | |
| <213> mouse | | | | |
| <220> | | | | |
| <221> CDS | | | | |
| <222> (7)..(813) | | | | |
| <220> | | | | |
| <221> mat_peptide | | | | |
| <222> (67)..(813) | | | | |
| <400> 31 | | | | |
| tctaga atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg | | | | 48 |
| Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala | | | | |
| | -20 | -15 | -10 | |
| gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag | | | | 96 |
| Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu | | | | |
| | -5 | -1 | 1 | 5 |
| | | | | 10 |
| ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc | | | | 144 |
| Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly | | | | |
| | 15 | 20 | 25 | |

| | |
|---|-----|
| tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg | 192 |
| Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val | |
| 30 35 40 | |
| cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act | 240 |
| His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr | |
| 45 50 55 | |
| gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa | 288 |
| Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys | |
| 60 65 70 | |
| tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac | 336 |
| Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp | |
| 75 80 85 90 | |
| tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg | 384 |
| Ser Ala Val Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly | |
| 95 100 105 | |
| act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga tct ggc tcc | 432 |
| Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser | |
| 110 115 120 | |
| gaa tcc aaa ccc ggg gat gtt gtg atg acc cca aac cca ctc tcc ctg | 480 |
| Glu Ser Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu | |
| 125 130 135 | |
| cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag | 528 |
| Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln | |
| 140 145 150 | |
| agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac ctg cag | 576 |
| Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln | |
| 155 160 165 170 | |
| aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga | 624 |
| Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg | |
| 175 180 185 | |
| ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat | 672 |
| Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp | |
| 190 195 200 | |
| ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat | 720 |
| Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr | |
| 205 210 215 | |
| ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc | 768 |
| Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr | |
| 220 225 230 | |
| aag ctg gaa ata aaa gaa gaa aaa ctc atc tca gaa gag gat ctg | 813 |
| Lys Leu Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu | |
| 235 240 245 | |
| aattagtaag cggccgc | 830 |

<210> 32
<211> 269

<212> PRT
 <213> mouse

<400> 32

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Ala | Ile | Val | Leu | Tyr | Val | Leu | Leu | Ala | Ala | Ala | Ala | His |
| -20 | | | | -15 | | | | | -10 | | | | | | -5 |
| Ser | Ala | Phe | Ala | Ala | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Leu | Val |
| | | | -1 | 1 | | | | 5 | | | | | 10 | | |
| Arg | Pro | Gly | Ala | Ser | Val | Thr | Leu | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr |
| | | 15 | | | | | 20 | | | | | 25 | | | |
| Phe | Thr | Asp | Tyr | Glu | Ile | His | Trp | Val | Arg | Gln | Thr | Pro | Val | His | Gly |
| | 30 | | | | | 35 | | | | | 40 | | | | |
| Leu | Glu | Trp | Ile | Gly | Ala | Ile | Asp | Pro | Glu | Thr | Gly | Gly | Thr | Ala | Tyr |
| 45 | | | | | 50 | | | | | 55 | | | | | 60 |
| Asn | Gln | Lys | Phe | Lys | Asp | Lys | Ala | Ile | Val | Thr | Val | Asp | Lys | Ser | Ser |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| Ser | Thr | Ala | Tyr | Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala |
| | | | 80 | | | | | 85 | | | | | 90 | | |
| Val | Tyr | Tyr | Tyr | Thr | Arg | Trp | Phe | Glu | Asp | Trp | Gly | Gln | Gly | Thr | Leu |
| | | 95 | | | | | 100 | | | | | 105 | | | |
| Val | Thr | Val | Ser | Ala | Glu | Gly | Lys | Ser | Ser | Gly | Ser | Gly | Ser | Glu | Ser |
| | 110 | | | | | 115 | | | | | 120 | | | | |
| Lys | Pro | Gly | Asp | Val | Val | Met | Thr | Pro | Asn | Pro | Leu | Ser | Leu | Pro | Val |
| 125 | | | | | 130 | | | | | 135 | | | | | 140 |
| Ser | Leu | Gly | Asp | Gln | Ala | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Gln | Ser | Leu |
| | | | | 145 | | | | | 150 | | | | | 155 | |
| Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | His | Trp | Tyr | Leu | Gln | Lys | Pro |
| | | | 160 | | | | | 165 | | | | | 170 | | |
| Gly | Gln | Ser | Pro | Lys | Leu | Leu | Ile | Tyr | Lys | Val | Ser | Asn | Arg | Phe | Ser |
| | | 175 | | | | | 180 | | | | | | 185 | | |
| Gly | Val | Pro | Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr |
| | 190 | | | | | 195 | | | | | | 200 | | | |
| Leu | Lys | Ile | Ser | Arg | Val | Glu | Ala | Glu | Asp | Leu | Gly | Val | Tyr | Phe | Cys |
| 205 | | | | | 210 | | | | | 215 | | | | | 220 |
| Ser | Gln | Ser | Thr | His | Val | Pro | Tyr | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu |
| | | | | 225 | | | | | 230 | | | | | 235 | |
| Glu | Ile | Lys | Glu | Glu | Lys | Leu | Ile | Ser | Glu | Glu | Asp | Leu | | | |
| | | | 240 | | | | | 245 | | | | | | | |

<210> 33
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:c-myc tag

 <400> 33
 gaagaaaaac tcatctcaga agaggatctg 30

 <210> 34
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:p67 leader

 <400> 34
 atggtaagcg ctattgtttt atatgtgctt ttggcggcgg cggcgcattc tgcctttgcg 60

 <210> 35
 <211> 84
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 35
 gcactaggtc aatctagaat gactatcctt tgctggctgg cccttctgtc aactctgact 60
 gccgtcaacg ctgcggttgt gatg 84

 <210> 36
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 36
 gcccttggtg ccctcgccgc tgcccggctt gccgctgccg ctggtgctgc cttttatttc 60
 cagcttggtc 70

 <210> 37
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 37
 ggcagcacca gcggcagcgg caagccgggc agcggcgagg gcagcaccaa gggccagggtt 60
 caactgcagc agtc 74

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<210> 38
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 38
gcactagggtc aagcggccgc atgatgatga tgatgatgag aaccccgcat tgcagagaca 60
gtgaccagag tc 72

<210> 39
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 39
aaaatttgcg gccgcctaat gatgatgatg atgatgagaa c 41

<210> 40
<211> 462
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (19)..(462)

<220>
<221> mat_peptide
<222> (73)...(462)

<400> 40
gcactagggtc aatctaga atg act atc ctt tgc tgg cta gcc ctt ctg tca 51
Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser
-15 -10

act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc 99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu
-5 -1 1 5

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
10 15 20 25

agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac 195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr
30 35 40

ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc 243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
45 50 55

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 291

```

| | | | | | | | | | | | | | | | | | |
|------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Arg | Phe | Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | | |
| | | 60 | | | | | 65 | | | | | 70 | | | | | |
| aca | gat | ttc | aca | ctc | aag | atc | agc | aga | gtg | gag | gct | gag | gat | ctg | gga | 339 | |
| Thr | Asp | Phe | Thr | Leu | Lys | Ile | Ser | Arg | Val | Glu | Ala | Glu | Asp | Leu | Gly | | |
| | 75 | | | | | 80 | | | | 85 | | | | | | | |
| gtt | tat | ttc | tgc | tct | caa | agt | aca | cat | gtt | ccg | tac | acg | ttc | gga | ggg | 387 | |
| Val | Tyr | Phe | Cys | Ser | Gln | Ser | Thr | His | Val | Pro | Tyr | Thr | Phe | Gly | Gly | | |
| | 90 | | | | 95 | | | | 100 | | | | | 105 | | | |
| ggg | acc | aag | ctg | gaa | ata | aaa | ggc | agc | acc | agc | ggc | agc | ggc | aag | ccg | 435 | |
| Gly | Thr | Lys | Leu | Glu | Ile | Lys | Gly | Ser | Thr | Ser | Gly | Ser | Gly | Lys | Pro | | |
| | | | | 110 | | | | 115 | | | | | | 120 | | | |
| ggc | agc | ggc | gag | ggc | agc | acc | aag | ggc | | | | | | | | 462 | |
| Gly | Ser | Gly | Glu | Gly | Ser | Thr | Lys | Gly | | | | | | | | | |
| | | | 125 | | | | | 130 | | | | | | | | | |
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| <210> 41 | | | | | | | | | | | | | | | | | |
| <211> 443 | | | | | | | | | | | | | | | | | |
| <212> DNA | | | | | | | | | | | | | | | | | |
| <213> mouse | | | | | | | | | | | | | | | | | |
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| <220> | | | | | | | | | | | | | | | | | |
| <221> CDS | | | | | | | | | | | | | | | | | |
| <222> (1)..(423) | | | | | | | | | | | | | | | | | |
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| <400> 41 | | | | | | | | | | | | | | | | | |
| ggc | agc | acc | agc | ggc | agc | ggc | aag | ccg | ggc | agc | ggc | gag | ggc | agc | acc | 48 | |
| Gly | Ser | Thr | Ser | Gly | Ser | Gly | Lys | Pro | Gly | Ser | Gly | Glu | Gly | Ser | Thr | | |
| | 1 | | | 5 | | | | 10 | | | | | | 15 | | | |
| aag | ggc | cat | gtt | caa | ctg | cag | cag | tct | ggg | gct | gag | ctg | gtg | agg | cct | 96 | |
| Lys | Gly | His | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Leu | Val | Arg | Pro | | |
| | | | 20 | | | | 25 | | | | | | 30 | | | | |
| ggg | gct | tca | gtg | acg | ctg | tcc | tgc | aag | gct | tcg | ggc | tac | aca | ttt | act | 144 | |
| Gly | Ala | Ser | Val | Thr | Leu | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | | |
| | | 35 | | | | 40 | | | | | | 45 | | | | | |
| gac | tat | gaa | ata | cac | tgg | gtg | aag | cag | aca | cct | gtg | cat | ggc | ctg | gaa | 192 | |
| Asp | Tyr | Glu | Ile | His | Trp | Val | Lys | Gln | Thr | Pro | Val | His | Gly | Leu | Glu | | |
| | 50 | | | | | 55 | | | | 60 | | | | | | | |
| tgg | att | gga | gct | att | gat | cct | gaa | act | ggt | ggt | act | gcc | tac | aat | cag | 240 | |
| Trp | Ile | Gly | Ala | Ile | Asp | Pro | Glu | Thr | Gly | Gly | Thr | Ala | Tyr | Asn | Gln | | |
| | 65 | | | | 70 | | | | 75 | | | | | 80 | | | |
| aag | ttc | aag | gac | aag | gcc | ata | gtg | act | gta | gac | aaa | tcc | tcc | agc | aca | 288 | |
| Lys | Phe | Lys | Asp | Lys | Ala | Ile | Val | Thr | Val | Asp | Lys | Ser | Ser | Ser | Thr | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| gcc | tac | atg | gag | ctc | cgc | agc | ctg | aca | tct | gaa | gac | tct | gcc | gtc | tat | 336 | |
| Ala | Tyr | Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | Tyr | | |
| | | | 100 | | | | 105 | | | | | | 110 | | | | |
| tac | tat | aca | aga | tgg | ttt | gag | gac | tgg | ggc | caa | ggg | act | ctg | gtc | act | 384 | |
| Tyr | Tyr | Thr | Arg | Trp | Phe | Glu | Asp | Trp | Gly | Gln | Gly | Thr | Leu | Val | Thr | | |
| | | 115 | | | | 120 | | | | | | 125 | | | | | |

| | |
|--|-----|
| gtc tct gca atg cgg ggt tct cat cat cat cat cat cat gcggccgctt | 433 |
| Val Ser Ala Met Arg Gly Ser His His His His His His | |
| 130 135 140 | |

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|------------|-----|
| gacctagtgc | 443 |
|------------|-----|

<210> 42
 <211> 851
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 <213> mouse

<220>
 <221> CDS
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<220>
 <221> mat_peptide
 <222> (73)..(831)

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| <400> 42 | |
| gcactagggtc aatctaga atg act atc ctt tgc tgg cta gcc ctt ctg tca | 51 |
| Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser | |
| -15 -10 | |

| | |
|---|----|
| act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc | 99 |
| Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu | |
| -5 -1 1 5 | |

| | |
|---|-----|
| tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct | 147 |
| Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser | |
| 10 15 20 25 | |

| | |
|---|-----|
| agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac | 195 |
| Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr | |
| 30 35 40 | |

| | |
|---|-----|
| ctg cag aag cca gcc cag tct cca aag ctc ctg atc tac aaa gtt tcc | 243 |
| Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser | |
| 45 50 55 | |

| | |
|---|-----|
| aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg | 291 |
| Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly | |
| 60 65 70 | |

| | |
|---|-----|
| aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga | 339 |
| Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly | |
| 75 80 85 | |

| | |
|---|-----|
| gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg | 387 |
| Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly | |
| 90 95 100 105 | |

| | |
|---|-----|
| ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag ccg | 435 |
| Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro | |
| 110 115 120 | |

| | |
|---|-----|
| ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag tct | 483 |
| Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln Ser | |
| 125 130 135 | |

| | |
|--|-----|
| ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag | 531 |
| Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys | |
| 140 145 150 | |
| gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg aag cag | 579 |
| Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Lys Gln | |
| 155 160 165 | |
| aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act | 627 |
| Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr | |
| 170 175 180 185 | |
| ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act | 675 |
| Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr | |
| 190 195 200 | |
| gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca | 723 |
| Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr | |
| 205 210 215 | |
| tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg | 771 |
| Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp | |
| 220 225 230 | |
| ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat cat | 819 |
| Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His His | |
| 235 240 245 | |
| cat cat cat cat gcggccgctt gacctagtgc | 851 |
| His His His His | |
| 250 | |
| <210> 43 | |
| <211> 867 | |
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| <222> (31)..(843) | |
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| <221> mat_peptide | |
| <222> (85)..(843) | |
| <400> 43 | |
| aatttaaacg gatcccggtt accttctaga atg act atc ctt tgc tgg cta gcc | 54 |
| Met Thr Ile Leu Cys Trp Leu Ala | |
| -15 | |
| ctt ctg tca act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca | 102 |
| Leu Leu Ser Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro | |
| -10 -5 -1 1 5 | |
| aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct | 150 |
| Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser | |
| 10 15 20 | |
| tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta | 198 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|------|-------|--------|------|------|-----|-----|-----|-----|-----|
| Cys | Arg | Ser | Ser | Gln | Ser | Leu | Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | |
| | | 25 | | | | | 30 | | | | | 35 | | | | |
| cat | tgg | tac | ctg | cag | aag | cca | ggc | cag | tct | cca | aag | ctc | ctg | atc | tac | 246 |
| His | Trp | Tyr | Leu | Gln | Lys | Pro | Gly | Gln | Ser | Pro | Lys | Leu | Leu | Ile | Tyr | |
| | 40 | | | | | 45 | | | | 50 | | | | | | |
| aaa | gtt | tcc | aac | cga | ttt | tct | ggg | gtc | cca | gac | agg | ttc | agt | ggc | agt | 294 |
| Lys | Val | Ser | Asn | Arg | Phe | Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Gly | Ser | |
| | 55 | | | | 60 | | | | | 65 | | | | | 70 | |
| gga | tca | ggg | aca | gat | ttc | aca | ctc | aag | atc | agc | aga | gtg | gag | gct | gag | 342 |
| Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Lys | Ile | Ser | Arg | Val | Glu | Ala | Glu | |
| | | | | 75 | | | | | 80 | | | | | 85 | | |
| gat | ctg | gga | gtt | tat | ttc | tgc | tct | caa | agt | aca | cat | gtt | ccg | tac | acg | 390 |
| Asp | Leu | Gly | Val | Tyr | Phe | Cys | Ser | Gln | Ser | Thr | His | Val | Pro | Tyr | Thr | |
| | | | 90 | | | | | 95 | | | | | 100 | | | |
| ttc | gga | ggg | ggg | acc | aag | ctg | gaa | ata | aaa | ggc | agc | acc | agc | ggc | agc | 438 |
| Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Gly | Ser | Thr | Ser | Gly | Ser | |
| | | 105 | | | | | 110 | | | | | 115 | | | | |
| ggc | aag | ccg | ggc | agc | ggc | gag | ggc | agc | acc | aag | ggc | cat | gtt | caa | ctg | 486 |
| Gly | Lys | Pro | Gly | Ser | Gly | Glu | Gly | Ser | Thr | Lys | Gly | His | Val | Gln | Leu | |
| | 120 | | | | | 125 | | | | | 130 | | | | | |
| cag | cag | tct | ggg | gct | gag | ctg | gtg | agg | cct | ggg | gct | tca | gtg | acg | ctg | 534 |
| Gln | Gln | Ser | Gly | Ala | Glu | Leu | Val | Arg | Pro | Gly | Ala | Ser | Val | Thr | Leu | |
| | | | | | 140 | | | | | 145 | | | | | 150 | |
| tcc | tgc | aag | gct | tcg | ggc | tac | aca | ttt | act | gac | tat | gaa | ata | cac | tgg | 582 |
| Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asp | Tyr | Glu | Ile | His | Trp | |
| | | | | 155 | | | | | 160 | | | | | 165 | | |
| gtg | aag | cag | aca | cct | gtg | cat | ggc | ctg | gaa | tgg | att | gga | gct | att | gat | 630 |
| Val | Lys | Gln | Thr | Pro | Val | His | Gly | Leu | Glu | Trp | Ile | Gly | Ala | Ile | Asp | |
| | | | 170 | | | | | 175 | | | | | 180 | | | |
| cct | gaa | act | ggt | ggt | act | gcc | tac | aat | cag | aag | ttc | aag | gac | aag | gcc | 678 |
| Pro | Glu | Thr | Gly | Gly | Thr | Ala | Tyr | Asn | Gln | Lys | Phe | Lys | Asp | Lys | Ala | |
| | | | 185 | | | | 190 | | | | | 195 | | | | |
| ata | gtg | act | gta | gac | aaa | tcc | tcc | agc | aca | gcc | tac | atg | gag | ctc | cgc | 726 |
| Ile | Val | Thr | Val | Asp | Lys | Ser | Ser | Ser | Thr | Ala | Tyr | Met | Glu | Leu | Arg | |
| | 200 | | | | | 205 | | | | | 210 | | | | | |
| agc | ctg | aca | tct | gaa | gac | tct | gcc | gtc | tat | tac | tat | aca | aga | tgg | ttt | 774 |
| Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | Tyr | Tyr | Tyr | Thr | Arg | Trp | Phe | |
| | 215 | | | | 220 | | | | | 225 | | | | | 230 | |
| gag | gac | tgg | ggc | caa | ggg | act | ctg | gtc | act | gtc | tct | gca | atg | cgg | ggg | 822 |
| Glu | Asp | Trp | Gly | Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ala | Met | Arg | Gly | |
| | | | | 235 | | | | 240 | | | | | | 245 | | |
| tct | cat | cat | cat | cat | cat | cat | tagg | cgccg | ctgcag | atct | gatc | | | | | 867 |
| Ser | His | His | His | His | His | His | | | | | | | | | | |
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<210> 44

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<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 44
tttaaaggcc atattggcca tgactatcct ttgctggct 39

<210> 45
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 45
tttaaaggcc atattggcca tggatgttgt gatgacccca aac 43

<210> 46
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 46
tttaaaggcc agagaggccc taatgatgat gatgatgatg agaaccccgc attg 54

<210> 47
<211> 882
<212> DNA
<213> mouse

<220>
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<220>
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<222> (79)..(837)

<400> 47
ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt 51
Met Thr Ile Leu Cys Trp Leu Ala Leu
-15 -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
-5 -1 1 5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
10 15 20

```

| | |
|---|-----|
| aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat | 195 |
| Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His | |
| 25 30 35 | |
| tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa | 243 |
| Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys | |
| 40 45 50 55 | |
| gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga | 291 |
| Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly | |
| 60 65 70 | |
| tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat | 339 |
| Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp | |
| 75 80 85 | |
| ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc | 387 |
| Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe | |
| 90 95 100 | |
| gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc | 435 |
| Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly | |
| 105 110 115 | |
| aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag | 483 |
| Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln | |
| 120 125 130 135 | |
| cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc | 531 |
| Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser | |
| 140 145 150 | |
| tgc aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg | 579 |
| Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val | |
| 155 160 165 | |
| agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct | 627 |
| Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro | |
| 170 175 180 | |
| gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata | 675 |
| Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile | |
| 185 190 195 | |
| gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc | 723 |
| Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser | |
| 200 205 210 215 | |
| ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag | 771 |
| Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Thr Arg Trp Phe Glu | |
| 220 225 230 | |
| gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct | 819 |
| Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser | |
| 235 240 245 | |
| cat cat cat cat cat tagggcctct ctggccgata cccgaattt | 867 |
| His His His His His | |
| 250 | |
| ccccgatcgt tcaaa | 882 |

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<220>
<221> CDS
<222> (25) .. (786)
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| ctgcagggta | cggccatatt | ggcc | atg | gat | gtt | gtg | atg | acc | cca | aac | cca | | | | | | 51 |
| | | | | | | | Met | Asp | Val | Val | Met | Thr | Pro | Asn | Pro | | |
| | | | | | | | 1 | | | | | 5 | | | | | |
| ctc | tcc | ctg | cct | gtc | agt | ctt | gga | gat | caa | gcc | tcc | atc | tct | tgc | aga | | 99 |
| Leu | Ser | Leu | Pro | Val | Ser | Leu | Gly | Asp | Gln | Ala | Ser | Ile | Ser | Cys | Arg | | |
| 10 | | | | | 15 | | | | | 20 | | | | | 25 | | |
| tct | agt | cag | agc | ctt | tta | cac | agt | aat | gga | atc | acc | tat | tta | cat | tgg | | 147 |
| Ser | Ser | Gln | Ser | Leu | Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | His | Trp | | |
| | | | | 30 | | | | | 35 | | | | | 40 | | | |
| tac | ctg | cag | aag | cca | ggc | cag | tct | cca | aag | ctc | ctg | atc | tac | aaa | gtt | | 195 |
| Tyr | Leu | Gln | Lys | Pro | Gly | Gln | Ser | Pro | Lys | Leu | Leu | Ile | Tyr | Lys | Val | | |
| | | | 45 | | | | | 50 | | | | | 55 | | | | |
| tcc | aac | cga | ttt | tct | ggg | gtc | cca | gac | agg | ttc | agt | ggc | agt | gga | tca | | 243 |
| Ser | Asn | Arg | Phe | Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Gly | Ser | Gly | Ser | | |
| | | 60 | | | | | 65 | | | | | 70 | | | | | |
| ggg | aca | gat | ttc | aca | ctc | aag | atc | agc | aga | gtg | gag | gct | gag | gat | ctg | | 291 |
| Gly | Thr | Asp | Phe | Thr | Leu | Lys | Ile | Ser | Arg | Val | Glu | Ala | Glu | Asp | Leu | | |
| 75 | | | | | | 80 | | | | | 85 | | | | | | |
| gga | gtt | tat | ttc | tgc | tct | caa | agt | aca | cat | gtt | ccg | tac | acg | ttc | gga | | 339 |
| Gly | Val | Tyr | Phe | Cys | Ser | Gln | Ser | Thr | His | Val | Pro | Tyr | Thr | Phe | Gly | | |
| 90 | | | | | 95 | | | | | 100 | | | | | 105 | | |
| ggg | ggg | acc | aag | ctg | gaa | ata | aaa | ggc | agc | acc | agc | ggc | agc | ggc | aag | | 387 |
| Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Gly | Ser | Thr | Ser | Gly | Ser | Gly | Lys | | |
| | | | | 110 | | | | 115 | | | | | | 120 | | | |
| ccg | ggc | agc | ggc | gag | ggc | agc | acc | aag | ggc | cat | gtt | caa | ctg | cag | cag | | 435 |
| Pro | Gly | Ser | Gly | Glu | Gly | Ser | Thr | Lys | Gly | His | Val | Gln | Leu | Gln | Gln | | |
| | | | 125 | | | | | 130 | | | | | 135 | | | | |
| tct | ggg | gct | gag | ctg | gtg | agg | cct | ggg | gct | tca | gtg | acg | ctg | tcc | tgc | | 483 |
| Ser | Gly | Ala | Glu | Leu | Val | Arg | Pro | Gly | Ala | Ser | Val | Thr | Leu | Ser | Cys | | |
| | | 140 | | | | | 145 | | | | | 150 | | | | | |
| aag | gct | tcg | ggc | tac | aca | ttt | act | gac | tat | gaa | ata | cac | tgg | gtg | agg | | 531 |
| Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asp | Tyr | Glu | Ile | His | Trp | Val | Arg | | |
| 155 | | | | | | 160 | | | | 165 | | | | | | | |
| cag | aca | cct | gtg | cat | ggc | ctg | gaa | tgg | att | gga | gct | att | gat | cct | gaa | | 579 |
| Gln | Thr | Pro | Val | His | Gly | Leu | Glu | Trp | Ile | Gly | Ala | Ile | Asp | Pro | Glu | | |
| 170 | | | | | 175 | | | | | 180 | | | | | 185 | | |
| act | ggt | ggt | act | gcc | tac | aat | cag | aag | ttc | aag | gac | aag | gcc | ata | gtg | | 627 |

| | |
|--|-----|
| Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val | |
| 190 195 200 | |
| act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg | 675 |
| Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu | |
| 205 210 215 | |
| aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac | 723 |
| Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp | |
| 220 225 230 | |
| tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat | 771 |
| Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His | |
| 235 240 245 | |
| cat cat cat cat cat tagggcctct ctggccgata ccccgaaattt ccccgatcgt | 826 |
| His His His His His | |
| 250 | |
| tcaaacattt ggcaataaag | 846 |

<210> 49
 <211> 738
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (19)..(687)
 <223> mature peptide is coded by nucleotides 49 to 687

| | |
|---|-----|
| <400> 49 | |
| cccggtacc cttctaga ctc gtg aca gtt gtt gat ggt gcc caa tcc cag | 51 |
| Leu Val Thr Val Val Asp Gly Ala Gln Ser Gln | |
| 1 5 10 | |
| gtt caa ctg cag cag tct ggg gct gag ctg gtg agg cct ggg gct tca | 99 |
| Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser | |
| 15 20 25 | |
| gtg acg ctg tcc tgc aag gct tcg ggc tac aca ttt act gac tat gaa | 147 |
| Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu | |
| 30 35 40 | |
| ata cac tgg gtg agg cag aca cct gtg cat ggc ctg gaa tgg att gga | 195 |
| Ile His Trp Val Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly | |
| 45 50 55 | |
| gct att gat cct gaa act ggt ggt act gcc tac aat cag aag ttc aag | 243 |
| Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys | |
| 60 65 70 75 | |
| gac aag gcc ata gtg act gta gac aaa tcc tcc agc aca gcc tac atg | 291 |
| Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met | |
| 80 85 90 | |
| gag ctc cgc agc ctg aca tct gaa gac tct gcc gtc tat tac tat aca | 339 |
| Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr | |
| 95 100 105 | |

| | |
|---|-----|
| aga tgg ttt gag gac tgg ggc caa ggg act ctg gtc act gtc tct gca | 387 |
| Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala | |
| 110 115 120 | |
| gcc aaa aca aca ccc cca tca gtc tat cca ctg gcc cct ggg tgt gga | 435 |
| Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Cys Gly | |
| 125 130 135 | |
| gat aca act ggt tcc tct gtg act ctg gga tgc ctg gtc aag ggc tac | 483 |
| Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr | |
| 140 145 150 155 | |
| ttc cct gag tca gtg act gtg act tgg aac tct gga tcc ctg tcc agc | 531 |
| Phe Pro Glu Ser Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser | |
| 160 165 170 | |
| agt gtg cac acc ttc cca gct ctc ctg cag tct gga ctc tac act atg | 579 |
| Ser Val His Thr Phe Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Met | |
| 175 180 185 | |
| agc agc tca gtg act gtc ccc tcc agc acc tgg cca agt cag acc gtc | 627 |
| Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val | |
| 190 195 200 | |
| acc tgc agc gtt gct cac cca gcc agc agc acc acg gtg gac aaa aaa | 675 |
| Thr Cys Ser Val Ala His Pro Ala Ser Ser Thr Thr Val Asp Lys Lys | |
| 205 210 215 | |
| ctt gag ccc agc gcggccgctg caggtcttga tcctttcctg ggacccggca | 727 |
| Leu Glu Pro Ser | |
| 220 | |
| agaaccaaaa a | 738 |
| <210> 50 | |
| <211> 42 | |
| <212> DNA | |
| <213> mouse | |
| <400> 50 | |
| gcactagggtc aagcggccgc ttactaacac tcattcctgt tg | 42 |
| <210> 51 | |
| <211> 753 | |
| <212> DNA | |
| <213> mouse | |
| <220> | |
| <221> CDS | |
| <222> (7)..(705) | |
| <220> | |
| <221> mat_peptide | |
| <222> (67)..(705) | |
| <400> 51 | |
| tctaga atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg | 48 |
| Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala | |
| -20 -15 -10 | |

| | |
|---|-----|
| gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag | 96 |
| Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu | |
| -5 -1 1 5 10 | |
| ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc | 144 |
| Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly | |
| 15 20 25 | |
| tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg | 192 |
| Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val | |
| 30 35 40 | |
| cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act | 240 |
| His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr | |
| 45 50 55 | |
| gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa | 288 |
| Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys | |
| 60 65 70 | |
| tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac | 336 |
| Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp | |
| 75 80 85 90 | |
| tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg | 384 |
| Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly | |
| 95 100 105 | |
| act ctg gtc act gtc tct gca gcc aaa aca aca ccc cca tca gtc tat | 432 |
| Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr | |
| 110 115 120 | |
| cca ctg gcc cct ggg tgt gga gat aca act ggt tcc tct gtg act ctg | 480 |
| Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu | |
| 125 130 135 | |
| gga tgc ctg gtc aag ggc tac ttc cct gag tca gtg act gtg act tgg | 528 |
| Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp | |
| 140 145 150 | |
| aac tct gga tcc ctg tcc agc agt gtg cac acc ttc cca gct ctc ctg | 576 |
| Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu | |
| 155 160 165 170 | |
| cag tct gga ctc tac act atg agc agc tca gtg act gtc ccc tcc agc | 624 |
| Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser | |
| 175 180 185 | |
| acc tgg acc tgc agc gtt gct cac cca gcc agc agc cca agt cag acc | 672 |
| Thr Trp Thr Cys Ser Val Ala His Pro Ala Ser Ser Pro Ser Gln Thr | |
| 190 195 200 | |
| gtc acc acg gtg gac aaa aaa ctt gag ccc agc tagtaatgag cggccgctgc | 725 |
| Val Thr Thr Val Asp Lys Lys Leu Glu Pro Ser | |
| 205 210 | |
| agatctgatac ctttctggg acccgga | 753 |

<210> 52

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nt 2253 to 2271
 of pDAB439

 <400> 52
 tgcattgtgtt ctccttttt 19

 <210> 53
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nt 4256 to 4308
 of pDAB439

 <400> 53
 ggtacggcca tattggccga gctcggcctc tctggccgat cccc 44

 <210> 54
 <211> 63
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nt 4744 to 4807
 of pDAB439

 <400> 54
 gcggccgctt taacgcccgg gcatttaaatt ggcgcgccgc gatcgcttgc agatctgcat 60
 ggg 63

 <210> 55
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:nt 5417 to 5436
 of pDAB439

 <400> 55
 ggggactcta gaggatccag 20

 <210> 56
 <211> 24
 <212> PRT
 <213> Zea mays

 <400> 56
 Pro Gly Ser Pro Ala Pro Ala Ala Pro Lys Asn Gly Leu Gly Glu Arg
 1 5 10 15

Pro Glu Ser Leu Asp Val Arg Gly
20